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RAW SEQUENCE LISTING

DATE: 04/25/2002

PATENT APPLICATION: US/09/828,068

TIME: 15:01:22

Input Set : A:\18941-14.app

Output Set: N:\CRF3\04252002\I828068.raw

ENTERED

C--> 3 <110> APPLICANT: Moon, Yong-Hwan
 4 Chen, Lingjing
 5 Sung, Zinmay R.
 7 <120> TITLE OF INVENTION: NUCLEIC ACIDS THAT CONTROL REPRODUCTIVE DEVELOPMENT IN
 8 PLANTS
 10 <130> FILE REFERENCE: 018941-001400US
 12 <140> CURRENT APPLICATION NUMBER: 09/828,068
 13 <141> CURRENT FILING DATE: 2002-04-11
 15 <160> NUMBER OF SEQ ID NOS: 2
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 3896
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Oryza sativa
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 33 tgtgcttgga ttgttgatgt gctaattcgc gccgttacaa gatcactgct ggattgatat 180
 35 tgagttgtgc ctgcgctgtg ctggctgtgt gttgattctc tcctcgtcgt ggtgatcgat 240
 37 atg gag att gtt gca gta gat cag gag gga gct cgt gtt gtt ggg acg 288
 38 Met Glu Ile Val Ala Val Asp Gln Glu Gly Ala Arg Val Val Gly Thr
 39 1 5 10 15
 41 aac tgt atg ctt gct cgt ggt gga act ggt gct gta gcg cca gtg ttg 336
 42 Asn Cys Met Leu Ala Arg Gly Gly Thr Gly Ala Val Ala Pro Val Leu
 43 20 25 30
 45 gag ctg aca gcg acg cct cgt cag gat gca gcc gct gaa gct ggt gta 384
 46 Glu Leu Thr Ala Thr Pro Arg Gln Asp Ala Ala Ala Glu Ala Gly Val
 47 35 40 45
 49 gac gaa ccg gca caa cac caa tgc gag cat ttc tcc ata aga ggg tat 432
 50 Asp Glu Pro Ala Gln His Gln Cys Glu His Phe Ser Ile Arg Gly Tyr
 51 50 55 60
 53 gtt gct ctt ctt cag aag gat cca aaa ttc tgc tct cta tct cgg 480
 54 Val Ala Leu Leu Gln Lys Lys Asp Pro Lys Phe Cys Ser Leu Ser Arg
 55 65 70 75 80
 57 att ttc cat gac cag aaa aaa tgt gat gaa cac aaa gct agt tca agc 528
 58 Ile Phe His Asp Gln Lys Lys Cys Asp Glu His Lys Ala Ser Ser Ser
 59 85 90 95
 61 cca ttt tct gta gca aag ttt cga cga tgg gat tgc tcg aag tgc ttg 576
 62 Pro Phe Ser Val Ala Lys Phe Arg Arg Trp Asp Cys Ser Lys Cys Leu
 63 100 105 110

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69 gca aag cag aat ggc aca agt gat ggt tgc tcc atc aca ttt gtt cgg 672
70 Ala Lys Gln Asn Gly Thr Ser Asp Gly Cys Ser Ile Thr Phe Val Arg
71      130      135      140
73 agc act ttt gtg cct gct agt gtt ggt tcc caa aaa gtg tct cct agc 720
74 Ser Thr Phe Val Pro Ala Ser Val Gly Ser Gln Lys Val Ser Pro Ser
75 145      150      155      160
77 aca caa tca tct caa ggg aag aat gct gat aga tca act ctt cca aag 768
78 Thr Gln Ser Ser Gln Gly Lys Asn Ala Asp Arg Ser Thr Leu Pro Lys
79      165      170      175
81 agt gtg caa gaa ggc aat gac tcc aaa tgc aat gcg cct tct ggc aag 816
82 Ser Val Gln Glu Gly Asn Asp Ser Lys Cys Asn Ala Pro Ser Gly Lys
83      180      185      190
85 aat gga gct gct gag gcc aat act gat tca cca atg aaa gat ttg caa 864
86 Asn Gly Ala Ala Glu Ala Asn Thr Asp Ser Pro Met Lys Asp Leu Gln
87      195      200      205
89 ggg cca gcc caa aat tat gat gtg gca gca aat gtc tct gag gac aac 912
90 Gly Pro Ala Gln Asn Tyr Asp Val Ala Ala Asn Val Ser Glu Asp Asn
91      210      215      220
93 act tct gtt gat gtt ggg gct tta cct gaa gtt ccc cag att aca tgg 960
94 Thr Ser Val Asp Val Gly Ala Leu Pro Glu Val Pro Gln Ile Thr Trp
95 225      230      235      240
97 cac ata gaa gta aat ggt gca gat caa cct cca tcc act cca aaa ctt 1008
98 His Ile Glu Val Asn Gly Ala Asp Gln Pro Pro Ser Thr Pro Lys Leu
99      245      250      255
101 tct gaa gtg gtc ctc aaa aga aat gaa gat gaa aat gga aaa act gaa 1056
102 Ser Glu Val Val Leu Lys Arg Asn Glu Asp Glu Asn Gly Lys Thr Glu
103      260      265      270
105 gag act ctt gtt gct gag cag tgc aat ttg acc aaa gat cct aac cca 1104
106 Glu Thr Leu Val Ala Glu Gln Cys Asn Leu Thr Lys Asp Pro Asn Pro
107      275      280      285
109 atg tct gga aag gaa cgt gat cag gtt gct gag cag tgc aat ttg acc 1152
110 Met Ser Gly Lys Glu Arg Asp Gln Val Ala Glu Gln Cys Asn Leu Thr
111      290      295      300
113 aaa gat ccg aaa cca gtg tct ggg cag aaa tgt gag cag atc tgc aat 1200
114 Lys Asp Pro Lys Pro Val Ser Gly Gln Lys Cys Glu Gln Ile Cys Asn
115 305      310      315      320
117 gag cca tgt gaa gaa gtt gtt ctc aaa aga agc tcc aaa tct aag agg 1248
118 Glu Pro Cys Glu Glu Val Val Leu Lys Arg Ser Ser Lys Ser Lys Arg
119      325      330      335
121 aag acg gat aag aag ttg atg aag aag cag cag cac agc aag aaa cgc 1296
122 Lys Thr Asp Lys Lys Leu Met Lys Lys Gln Gln His Ser Lys Lys Arg
123      340      345      350
125 act gcc cag gct gat gtt tca gat gca aag ctt tgt cgg aga aag cca 1344
126 Thr Ala Gln Ala Asp Val Ser Asp Ala Lys Leu Cys Arg Arg Lys Pro
127      355      360      365
129 aaa aag gtg cgg ctt cta tca gaa att ata aat gct aac cag gtt gag 1392

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134 Asp Ser Arg Ser Asp Glu Val His Arg Glu Asn Ala Ala Asp Pro Cys
135 385      390      395      400
137 gag gat gat aga agt acc atc ccg gtc ccg atg gaa gta agc atg gat 1488
138 Glu Asp Asp Arg Ser Thr Ile Pro Val Pro Met Glu Val Ser Met Asp
139      405      410      415
141 att cct gtt agc aac cat aca gtg gga gaa gat ggg tta aaa tca agt 1536
142 Ile Pro Val Ser Asn His Thr Val Gly Glu Asp Gly Leu Lys Ser Ser
143      420      425      430
145 aag aac aag aca aaa cgc aaa tac tct gat gtt gta gat gat gga tca 1584
146 Lys Asn Lys Thr Lys Arg Lys Tyr Ser Asp Val Val Asp Asp Gly Ser
147      435      440      445
149 tca ctt atg aac tgg ctg aat gga aaa aag aaa aga act gga agt gtg 1632
150 Ser Leu Met Asn Trp Leu Asn Gly Lys Lys Lys Arg Thr Gly Ser Val
151      450      455      460
153 cat cac aca gtt gct cat cca gct ggg aat ttg agc aac aaa aaa gtg 1680
154 His His Thr Val Ala His Pro Ala Gly Asn Leu Ser Asn Lys Lys Val
155 465      470      475      480
157 aca ccc act gcg agt act cag cat gat gat gag aat gat act gaa aat 1728
158 Thr Pro Thr Ala Ser Thr Gln His Asp Asp Glu Asn Asp Thr Glu Asn
159      485      490      495
161 ggt ctt gac aca aat atg cat aag aca gat gtc tgt cag cat gta tca 1776
162 Gly Leu Asp Thr Asn Met His Lys Thr Asp Val Cys Gln His Val Ser
163      500      505      510
165 gaa atc tcc aca cag agg tgc tca tca aag ggg aaa aca gcg ggt ttg 1824
166 Glu Ile Ser Thr Gln Arg Cys Ser Ser Lys Gly Lys Thr Ala Gly Leu
167      515      520      525
169 agt aag ggg aaa aca cat tca gct gct agt acc aaa tat ggt ggt gaa 1872
170 Ser Lys Gly Lys Thr His Ser Ala Ala Ser Thr Lys Tyr Gly Gly Glu
171      530      535      540
173 agc acc aga aat ggt cag aac ata cat gta ctc agc gca gaa gat caa 1920
174 Ser Thr Arg Asn Gly Gln Asn Ile His Val Leu Ser Ala Glu Asp Gln
175 545      550      555      560
177 tgc cag atg gaa acc gaa aac tct gtt ctg agt cac tcg gca aag gtt 1968
178 Cys Gln Met Glu Thr Glu Asn Ser Val Leu Ser His Ser Ala Lys Val
179      565      570      575
181 tct cca gct gag cat gat atc caa att atg tct gac ctt cat gag cag 2016
182 Ser Pro Ala Glu His Asp Ile Gln Ile Met Ser Asp Leu His Glu Gln
183      580      585      590
185 agt cta ccc aag aag aaa aag aag caa aaa ctt gaa gtg act cgt gaa 2064
186 Ser Leu Pro Lys Lys Lys Lys Lys Gln Lys Leu Glu Val Thr Arg Glu
187      595      600      605
189 aaa cag acc atg ata gat gac atc ccc atg gat att gtt gaa ctg cta 2112
190 Lys Gln Thr Met Ile Asp Asp Ile Pro Met Asp Ile Val Glu Leu Leu
191      610      615      620
193 gct aaa aac cag cat gag agg cag ctt atg act gag act gat tgt tct 2160
194 Ala Lys Asn Gln His Glu Arg Gln Leu Met Thr Glu Thr Asp Cys Ser

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198	Asp Ile Asn Arg Ile Gln Ser Lys Thr Thr Ala Asp Asp Asp Cys Val							
199			645		650		655	
201	ata gta gct gcc aag gat ggt tca gat tat gca tca agt gtg ttt gac	2256						
202	Ile Val Ala Ala Lys Asp Gly Ser Asp Tyr Ala Ser Ser Val Phe Asp							
203			660		665		670	
205	act aat tcc caa cag aag tcc ttg gca tcc caa agt aca cag aag gag	2304						
206	Thr Asn Ser Gln Gln Lys Ser Leu Ala Ser Gln Ser Thr Gln Lys Glu							
207			675		680		685	
209	tta cag ggt cat ttg gca ttg acc aca caa gag tct cca cat cct cag	2352						
210	Leu Gln Gly His Leu Ala Leu Thr Thr Gln Glu Ser Pro His Pro Gln							
211			690		695		700	
213	aac ttt cag tct act cag gaa cag cag aca cat ttg cgg atg gaa gaa	2400						
214	Asn Phe Gln Ser Thr Gln Glu Gln Gln Thr His Leu Arg Met Glu Glu							
215	705		710		715		720	
217	atg gtc act att gct gca agc tca cca cta ttt tca cat cat gat gat	2448						
218	Met Val Thr Ile Ala Ala Ser Ser Pro Leu Phe Ser His His Asp Asp							
219			725		730		735	
221	cag tat att gct gaa gca cca act gaa cat tgg ggc cgt aag gac gca	2496						
222	Gln Tyr Ile Ala Glu Ala Pro Thr Glu His Trp Gly Arg Lys Asp Ala							
223			740		745		750	
225	aag aag cta acg tgg gag caa ttt aag gcc act aca aga aat tct cca	2544						
226	Lys Lys Leu Thr Trp Glu Gln Phe Lys Ala Thr Thr Arg Asn Ser Pro							
227			755		760		765	
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230	Ala Ala Thr Cys Gly Ala Gln Phe Arg Pro Gly Ile Gln Ala Val Asp							
231			770		775		780	
233	ttg act tct act cat gtc atg gga tct tcc agc aat tat gca tct cgc	2640						
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235	785		790		795		800	
237	caa cca gta att gcg cca ctg gac cgc tat gct gaa aga gcg gtt aac	2688						
238	Gln Pro Val Ile Ala Pro Leu Asp Arg Tyr Ala Glu Arg Ala Val Asn							
239			805		810		815	
241	cag gtc cat gca aga aat ttt cca agc aca ata gca acc atg gaa gcg	2736						
242	Gln Val His Ala Arg Asn Phe Pro Ser Thr Ile Ala Thr Met Glu Ala							
243			820		825		830	
245	agt aag tta tgt gat cgg aga aat gct gga caa gta gtc ttg tat cct	2784						
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247			835		840		845	
249	aaa gaa tcc atg cct gcg acg cat ctt ctg aga atg atg gat cca tca	2832						
250	Lys Glu Ser Met Pro Ala Thr His Leu Leu Arg Met Met Asp Pro Ser							
251			850		855		860	
253	aca tta gca agc ttc ccc aac tat gga act tct agc agg aac cag atg	2880						
254	Thr Leu Ala Ser Phe Pro Asn Tyr Gly Thr Ser Ser Arg Asn Gln Met							
255	865		870		875		880	
257	gag tct caa ctt cat aat tct cag tat gca cat aat cag tac aaa gga	2928						
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259			885		890		895	

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266 Thr Phe Glu Asp Leu Ser Arg His Gln Leu His Asp Leu His Arg Pro
267          915          920          925
269 tta cgc cca cat cct aga gtt ggt gtg ctt ggc tcc ttg ctg cag aag 3072
270 Leu Arg Pro His Pro Arg Val Gly Val Leu Gly Ser Leu Leu Gln Lys
271          930          935          940
273 gaa att gca aac tgg tcg gag aac tgt ggc aca caa tct ggt tat aag 3120
274 Glu Ile Ala Asn Trp Ser Glu Asn Cys Gly Thr Gln Ser Gly Tyr Lys
275 945          950          955          960
277 tta gga gtg tca aca gga ata aca tcg cat cag atg aac aga aag gaa 3168
278 Leu Gly Val Ser Thr Gly Ile Thr Ser His Gln Met Asn Arg Lys Glu
279          965          970          975
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283          980          985          990
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286 Leu Gln Leu Gly Ser Val Ser Ser Ser Ala Asp Phe Leu Ser Ala Arg
287          995          1000          1005
289 aac agc ata gct caa tct tgg acc aga ggc aag ggt aaa atg gtt cat 3312
290 Asn Ser Ile Ala Gln Ser Trp Thr Arg Gly Lys Gly Lys Met Val His
291          1010          1015          1020
293 ccc ttg gat cgg ttt gtg aga cag gat atc tgt ata act aac aag aac 3360
294 Pro Leu Asp Arg Phe Val Arg Gln Asp Ile Cys Ile Thr Asn Lys Asn
295          1025          1030          1035          1040
297 cca gct gat ttt act aca atc agt aac gat aac gag tat atg gat tac 3408
298 Pro Ala Asp Phe Thr Thr Ile Ser Asn Asp Asn Glu Tyr Met Asp Tyr
299          1045          1050          1055
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302 Arg
304 tcattctttat ggcgccaaat agtcatactg taagaggagg gctttgctgg atctgctgta 3521
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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date